OM protein - protein search, using sw model

```
                                  GenCore version 4.5
                              Copyright (c) 1993 - 2000 Compugen Ltd.

Run on:                 May  7, 2002, 15:11:37 ; Search time 0.29 Seconds
                                                 (without alignments)
                                                 4.216 Million cell updates/sec

Title:                  us-09-783-320-6
Perfect score:          5162
Sequence:               1 MKNLVLKIISGSFPPVSLHY........YAKILHLVMADGAYQEDNDE 1007

Scoring table:          BLOSUM62
                        Gapop 10.0 , Gapext 0.5

Searched:               1 seqs, 1214 residues

Total number of hits satisfying chosen parameters:          1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :              us-09-783-320-4:*


Pred. No: is the number of results predicted by chance to have a
          score greater than or equal to the score of the result being printed,
          and is derived by analysis of the total score distribution.


                                  SUMMARIES

Result                  Query
No.     Score   Match   Length DB  ID                      Description
------  -----   -----   ------ --- --                      -----------
1       5162    100.0   1214   1   us-09-783-320-4


                                  ALIGNMENTS

RESULT  1
us-09-783-320-4

Query Match             100.0%;  Score 5162;  DB 1;  Length 1214;
Best Local Similarity   100.0%;
Matches  1007;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;


Qy       1 MKNLVLKIISGSFPPVSLHYSYDLRSLVSSQLFKRNPRDRPSVNSILEKGFIAKRIEKFLS 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     208 MKNLVLKIISGSFPPVSLHYSYDLRSLVSSQLFKRNPRDRPSVNSILEKGFIAKRIEKFLS 267

Qy      61 PQLIAEEFCLKTFSKFGSQPIPAKRPASGQNSISVMPAQKITKPAAKYGIPLAYKKYGDK 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     268 PQLIAEEFCLKTFSKFGSQPIPAKRPASGQNSISVMPAQKITKPAAKYGIPLAYKKYGDK 327

Qy     121 KLHEKKPLQKHKQAHQTPEKRVNTGEERRKISEEAARKRLEFIEKEKKQKDQIISLMKA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     328 KLHEKKPLQKHKQAHQTPEKRVNTGEERRKISEEAARKRLEFIEKEKKQKDQIISLMKA 387

Qy     181 EQMKROEKERLERINRAREQGWRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGQYEHYH 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     388 EQMKROEKERLERINRAREQGWRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGQYEHYH 447

Qy     241 AIFDQMQOQRAEDNEAKWKREIYGRGLPEROKGQLAVERAKQVEEFLQRKREAMQNKARA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     448 AIFDQMQOQRAEDNEAKWKREIYGRGLPEROKGQLAVERAKQVEEFLQRKREAMQNKARA 507

Qy     301 EGHMVYLARLRQIRLQNENEROQIKAKLRGEKKEANHSEGOEGSEEADMRRKKIESLKAH 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     508 EGHMVYLARLRQIRLQNENEROQIKAKLRGEKKEANHSEGOEGSEEADMRRKKIESLKAH 567

Qy     361 ANARAAVLKEQLERKRKEAYEREKKVWEEHLVAKGVKSSDVSPPLGQHETGGSPSKQQMR 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     568 ANARAAVLKEQLERKRKEAYEREKKVWEEHLVAKGVKSSDVSPPLGQHETGGSPSKQQMR 627

Qy     421 SVISVTSALKEVGVDSSLTDTRETSEEMQKTNNAISSKREILRRLNENLKAQEDEKGMON 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     628 SVISVTSALKEVGVDSSLTDTRETSEEMQKTNNAISSKREILRRLNENLKAQEDEKGMON 687

Qy     481 LSDTFEINVHEDAKEHEKEKSVSSDRKKWEAGGOLVIPLDELTLDTSFSTTERHTVGEVI 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     688 LSDTFEINVHEDAKEHEKEKSVSSDRKKWEAGGOLVIPLDELTLDTSFSTTERHTVGEVI 747

Qy     541 KLGPNGSPRRAWGKSPTDSVLKIIGEAELQLQTELLENTTIRSEISPEGEKYKPLITGEK 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     748 KLGPNGSPRRAWGKSPTDSVLKIIGEAELQLQTELLENTTIRSEISPEGEKYKPLITGEK 807

Qy     601 KVQCISHEINPSAIVDSPVETKSPEFSEASPQMSLKLEGNLEEPDDLETEILQOEPSGTNK 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     808 KVQCISHEINPSAIVDSPVETKSPEFSEASPQMSLKLEGNLEEPDDLETEILQOEPSGTNK 867

Qy     661 DESLPCITTDVWISEEKETKETQSADRITIOENEVSEDGVSSTVDQLSDIHIEPGTNDSQ 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     868 DESLPCITTDVWISEEKETKETQSADRITIOENEVSEDGVSSTVDQLSDIHIEPGTNDSQ 927

Qy     721 HSKCDVDKSVQPEPFFHKVVHSEHLNLVPOVQSVQOCSPEESFAFRSHSHLPPKNKNSL 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     928 HSKCDVDKSVQPEPFFHKVVHSEHLNLVPOVQSVQOCSPEESFAFRSHSHLPPKNKNSL 987

Qy     781 LIGLSTGLFDANNPKMLRTCSLPDLSKLFRTLMDVPTVGDVRQDNLEIDEIKDENIKEGP 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     988 LIGLSTGLFDANNPKMLRTCSLPDLSKLFRTLMDVPTVGDVRQDNLEIDEIKDENIKEGP 1047

Qy     841 SDSEDIVFEETDTDLQOELQOASMEQLLREQPGEEYSEEEESVLKNSDVEPTANGTDVADED 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1048 SDSEDIVFEETDTDLQOELQOASMEQLLREQPGEEYSEEEESVLKNSDVEPTANGTDVADED 1107

Qy     901 DNPSSESALNEEWHSDNSDGEIASSECECDSVFNHLEELRLHLEQEMGFEKFFEVYEKIKA 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1108 DNPSSESALNEEWHSDNSDGEIASSECECDSVFNHLEELRLHLEQEMGFEKFFEVYEKIKA 1167

Qy     961 IHEDEDENIEICSKIVQNILGNEHQHLYAKILHLVMADGAYQEDNDE 1007
           ||||||||||||||||||||||||||||||||||||||||||||||
Db    1168 IHEDEDENIEICSKIVQNILGNEHQHLYAKILHLVMADGAYQEDNDE 1214


Search completed: May  7, 2002, 15:11:39
Job time: 2 sec
```

OM nucleic - nucleic search, using sw model

GenCore version 4.5
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Run on: May   7, 2002, 15:09:25 ; Search time 5.77 Seconds
                                            (without alignments)
                                            3.821 Million cell updates/sec

Title: us-09-783-320-5
Perfect score: 3024
Sequence: 1 atgaaaaacctggtactgaa..................aagaagataatgatgaataa 3024

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 3645 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   us-09-783-320-3:*

              Pred. No. is the number of results predicted by chance to have a
              score greater than or equal to the score of the result being printed,
              and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query	Match Length	DB	ID	Description
1	3024	100.0	3645	1	us-09-783-320-3	
2	28.8	1.0	3645	1	us-09-783-320-3	

ALIGNMENTS

RESULT   1
us-09-783-320-3

Query Match   100.0%; Score 3024; DB 1; Length 3645;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 3024; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy     1 atgaaaaacctggtactgaagaatatatctgtatctcttccacctgtcttcttgcatat 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   622 atgaaaaacctggtactgaagaatatatctgtatctcttccacctgtcttcttgcatat 681

Qy    61 tcctatgatctccgcagtttggtctcagttattattttaaagagaatcctaggatagacca 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   682 tcctatgatctccgcagtttggtctcagttattattttaaagagaatcctaggatagacca 741

Qy   121 tcagtcaactccatattggagaaaggtttatagccaaacgcattgaaaagttctctct 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   742 tcagtcaactccatattggagaaaggtttatagccaaacgcattgaaaagttctctct 801

Qy   181 cctcagcttattgcaaaagaatatttgtctaaaaacatctttcaagtttggatcaacagct 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   802 cctcagcttattgcagaagaatttgtctaaaaacatttccgaagtttaactacttaactgat 861

Qy   241 ataccagctaaagaccaagcttcaggacaaaactcgattctgttatgctgctcagaaa 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   862 ataccagctaaagaccaagcttcaggacaaaactcgattctgttatgctgctcagaaa 921

Qy   301 attacaaaagcctgccgctaaatatggaatcacctttagcatataagaacatatgggagataa 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   922 attacaaaagcctgccgctaaatatggaatcacctttagcataaagaacatatgggagataa 981

Qy   361 aaattacacgaaaagaaaccactgcaaaaacatgaatactcttagcataaagaatatggagataa 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   982 aaattacacgaaaagcctgccaaatatggaatactcttagcataaagaatatggagataa 1041

Qy   421 agagtgaatactgaagaaaaggagagaaaccactgcaaaaacaataaacacataaacaaggaag 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1042 agagtgaatactgaagaaaaggagagaaaccactgcaaaaacaataaacacataaacaaggaag 1101

Qy   481 ctggaatttattgaaaagaacaacaaaagaaggatcagattattaagttaatgaaggct 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1102 ctggaatttattgaaaagaacaacaaaagaaggatcagattattaagttaatgaaggct 1161

Qy   541 gaacaaaatgaaaaggcaagaaaaggcaagaaaaggttgggaagaataaatatagggccaggggaaca 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1162 gaacaaaatgaaaaggcaagaaaaggcaagaaaaggttgggaagaataaatatagggccaggggaaca 1221

Qy   601 ggatggagaaatgtgctaagtgtcggttggaagtgaagttcctttctgggc 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1222 ggatggagaaatgtgctaagtgtcggttggaagtgaagttcctttctgggc 1281

Qy   661 agtggaaggggactatagctccatcatctcttttcttctcgaggacagagttgaacattaccat 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1282 agtggaggggactatagctccatcatctcttttcttctcgaggacagagttgaacattaccat 1341

Qy   721 gccattttgaccaaaagtgcagcacaaagcagaagaataatgaagagctaaatgaaaga 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1342 gccattttgaccaaaagtgcagcacaaagcagagaataatgaagagctaaatgaaaaga 1401

Qy   781 gaaatatatggtcgaggtcttccagaaaggcaaaaagggcagctagaaagaaaggagct 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1402 gaaatatatggtcgaggtcttccagaaaggcaaaaagggcagctagactgtagaaaagct 1461

Qy   841 aaacaagtagaagagttcctgcagacgaaaacggaagctatgcagaataaagctcagcc 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1462 aaacaagtagaagagttcctgcagacgaaaacggaagctatgcagaataaagctcagcc 1521

Qy   901 gaaggacatatgtgttatctgcaagactgaggcaaataggactacagaattcatgag 960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1522 gaaggacatatgtgttatctgcaagactgaggcaaataggactacagaattcatgag 1581

Qy   961 cgccaacagattaaagccaaacttcgttggtgaaagaaagaagctaatcattctgaaga 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1582 cgccaacagattaaagccaaacttcgttggtgaaagaaagaagctaatcattctgaaga 1641

Qy  1021 caagaaaggaagtgaaagaagctgaagagcgcaaaaatcgaatcactgaagcgcccat 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1642 caagaaggaagtgaaagaagctgaagagcgcaaaaatcgaatcactgaagcgcccat 1701

Qy  1081 gcaaatgcacgtgctgctgtactaaagaagacaactgaaaaagaacgaaagaagagcttat 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1702 gcaaatgcacgtgctgctgtactaaagaagacaactgaaaaagaacgaaagaagagcttat 1761

Qy  1141 gagagagaaaaaaagtgtgggaaggagcattttggttggctaaagggttaagagttctgat 1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1762 gagagagaaaaaaagtgtgggaaggagcattttggttggctaaagggttaagagttctgat 1821

Qy  1201 gttctctccacctttggggacgctgactccatcaaagcaacaagatgaga 1260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1822 gttctctccacctttggggacgctgactccatcaaagcaacaagatgaga 1881

Qy  1261 tctgttattctgtaacttcagctttgaacgaagttcgtggacgtagttaactgat 1320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1882 tctgttattctgtaacttcagctttgaacgaagttcgtggacgtagttaactgat 1941

Qy  1321 accgggaaaacttcagagagacaacaatgctattcaagtaagcgagaa 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1942 accgggaaacttcagagagacaacaatgctattcaagtaagcgagaa 2001
```

Qy 1381 atacttcgcagagattaaatcttaaagctcaagagatgaaaagggaatgcagagat 1440
Db 2002 atacttcgcagagattaaatgatgaaaatcttaaagctcaagagatgaaaaggaatgcagat 2061

Qy 1441 ctcctcgatatactttgaagataaagtgttcatgaagatcgaagatcgcaagagagcatgaaaaagcatga 1500
Db 2062 ctctcgatatactttgagataaagttcatgaagatcgaagagcatgaagcatgaaaagaagaaaa 2121

Qy 1501 tcagttcactgatcgcaagagtggggagtcaggaggtcaacttgattcctctggat 1560
Db 2122 tcagttcatctgatcgcaagagtggggaggcaggaggtcaacttgattcctctggat 2181

Qy 1561 gagttaacactagatacaatcctctctacaactacaacttgatgaagttatt 1620
Db 2182 gagttaacactagatacaatcctctctacaactacaacttgatgaagttatt 2241

Qy 1621 aaaattaggtcctaatggatcttccagagaagctgggggaagtccgacacagaatctcgtt 1680
Db 2242 aaaattaggtcctaaaggatccatcctctctacaactacaacttggatgaagttatt 2301

Qy 1681 ctaaagatacttggggaaggctgaactgcccaagagagctgggggaagtccgacacagaatctcgtt 1740
Db 2302 ctaaagatacttggggaagctgaactacccagagaagctgggggaagtccgacacagaatctcgtt 2361

Qy 1741 attagaaagtgagattctccgaaggggaaaagtacaaacctccttgaattactggagaaaa 1800
Db 2362 attagaaagtgagattctccgaaggggaaaagtacaaacctccttggagaaaa 2421

Qy 1801 aaagtacaatgtgattctcacatgaaatcagctattgttgattctctgttgag 1860
Db 2422 aaagtacaatgtattctcacatgaaatcagctattgttgattctctgttgag 2481

Qy 1861 acaaaaaagtcccggagttcagtgagtgcatccacagatgtcattgaaactggaagaaat 1920
Db 2482 acaaaaaagtcccggagttcagtgagtgcatccacagatgtcattgaaactggaagaaat 2541

Qy 1921 ttagaagaacctgatcgattggaaacagaaattctacacagagcaacccagtgaacaaacaa 1980
Db 2542 ttagaagaacctgatcgattggaaacagaaattctacacagagcaacccagtgaacaaacaa 2601

Qy 1981 gatgagagctgcacaatccatgcactattactgatcgtgtggattagtgagggaaaagaaacaaag 2040
Db 2602 gatgagagctgcacaatccatgcactattactgatcgtgtggattagtgagggaaaagaaacaaag 2661

Qy 2041 gaaactcagtcggcagataggacatccaattcaggagaaaatgaagttctgaagatggagtc 2100
Db 2662 gaaactcagtcggcagataggacatccaattcaggagaaaatgaagttctgaagatggagtc 2721

Qy 2101 tcgagtactgtggaccaacttgacattccatatagagcctggaaccaatgagattctcag 2160
Db 2722 tcgagtactgtggaccaacttgacattcatataagagcctggaaccaatgagattctcag 2781

Qy 2161 cactcctaaaatgtgtgatgataagtctgtcgcaaccggaaccacattttccaatggtt 2220
Db 2782 cacctaaatgtgatgtagataagtctgtcgcaaccggaaccacatttttccaataagtgtt 2841

Qy 2221 catctgaacacttagtccctcaagttcaatcagtgttccaccagagaa 2280
Db 2842 cattctgaacacttagtccctcaagttcaatcagtgttccaccagagaa 2901

Qy 2281 tccttgcatttcgatctcactccgatctacacacaaaatagaaacaagaattccttg 2340
Db 2902 tccttgcatttcgatctcactccgcatttacacacaaaaataaaacaagaattccttg 2961

Qy 2341 ctgattggacttcaactcgtctgtttgatcgatgcaaacaaccaaagatgttaaggacactgt 2400
Db 2962 ctgattggacttcaactcgtctgtttgatcgaaacaaccaaagatgttaaggacactgt 3021

Qy 2401 tcacttccagatctccaaagctgttcagagaacccttatggatgttcccacgtaggagat 2460
Db 3022 tcacttccagatctccaaagctgttcagagaacccttatggatgttcccacgtaggagat 3081

Qy 2461 gtccgttcaagacaatcttgaaaatagtagatgaatttaaagatgaaaacattaaagatgaaggact 2520
Db 3082 gtccgttcaagacaatcttgaaaatagtagatgaatttaaagatgaaaacattaaagatgaaggacct 3141

Qy 2521 tctgattctgaagacattgtgtttgaagaaactgacacagatttacaaggagctgcaggcc 2580
Db 3142 tctgattctgaagacattgtgtttgaagaaactgacacagatttacaaggagctgcaggcc 3201

Qy 2581 tcgatggaacagttcacttagggaacaacctgtgaagtactaaaggagaagaagaagaagtca 2640
Db 3202 tcgatggaacagttacttcagggaacaacctgtgaagtactacagaggaagaagaagagtca 3261

Qy 2641 gtcctgaagacacgtgtgggggccaaactgcaaatggggacagtgtgcagatgaagat 2700
Db 3262 gtcttgaagacacgtgatggtgggggccaaactgcaaatggggacagtgtggcagatgaagat 3321

Qy 2701 gacaatcccagtagtgacagaagtgccctgaacgaagaagtgcactccagaataacaagtgatggt 2760
Db 3322 gacaatcccagtagtgacagaagtgccctgaacgaagaagtgcactccagaataacaagtgatggt 3381

Qy 2761 gaaattgtagttgaatgtgaatcgatagtgtcttaaccattagaggagaagaactgagact 2820
Db 3382 gaaattgctagttgaatgtgaatcgatagtgtcttaaccattagaggagaagaactgagact 3441

Qy 2821 catctggagcaggagaaatgggcttgaaaaattcttgaaaattgtgagaaaataaaaggct 2880
Db 3442 catctggagcaggagaaatgggcttgaaaaatttcttgaaaaagtttatgagaaaataaaaggct 3501

Qy 2881 ggaaatgaacatcagcacatctcttatgccaagatctcattaagttcatttgcagatggaatt 2940
Db 3502 ggaaatgaacatcagcacatctcttatgccaagatctcattaagttcatttgcagatggaatt 3561

Qy 2941 ggaaatgaacatcagcacatctcttatgccaagatctcattaagttcatttgcagatggagcc 3000
Db 3562 ggaaatgaacatcagcacatctcttatgccaagatctcattaagttcatttgcagatggagcc 3621

Qy 3001 taccaagaaagataatgatgaataa 3024
Db 3622 taccaagaagataatgatgaataa 3645

Query Match   Best Local Similarity   53.6%;   Score 28.8;   DB 1;   Length 3645;
Matches   60;   Conservative   0;   Mismatches   52;   Indels   0;   Gaps   0;
Pred. No.   0;

Qy 2869 aaaataaggctattcatgaagatgaaaatatgaaaattggtcaaaatagtt 2928
Db 3601 AATGAGAACAATCTTGGGCATAAAGAATGCTCAATGTTCATTTCCCAAAATATATTTTTGAACTATTT 3542

Qy 2929 caaaatatttttgggaaatgaacatcagcacatcttatgccaagatcttcatt 2980
Db 3541 TTGAACAAAATTTCAATATATTTCAATCTTCATCTTYCATGAATAGCCTTTATTTT 3490

Search completed: May 7, 2002, 15:09:42
Job time: 17 sec

align_5_3   Page 2